

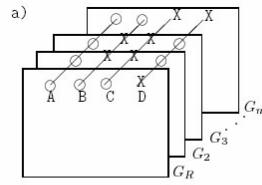
## Overview: Landmark

### Landmarking Program to Create/Edit Landmark Points Between Samples

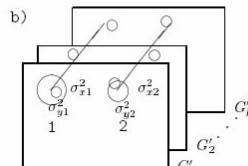
<http://open2dprot.sourceforge.net/Landmark>

Revised: 04-29-2005, P. Lemkin, G. Thornwall

### Composite Samples Database (CSD) Paradigm



Proteomic composite samples database (CSD) consisting of a set of n samples  $G_1, G_2, \dots, G_n$  with representative sample  $G_R = G_1$



A canonical sample database is a statistical representation of the CSD spot geometry and quantification that could be used for data mining

in Lemkin et al.,  
Computers Biomedical Research, 1981

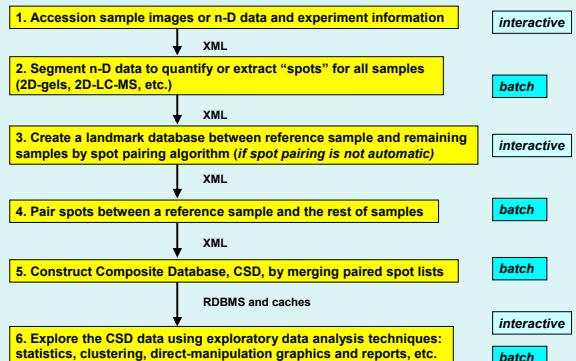
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### Introduction

- Spot pairing between spots from two samples may require a small set of corresponding spots known to be the same in the two samples.
- Some pairing programs require landmark data.
- Set of landmark points must be created prior to spot pairing and are stored in a landmark database.

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### Basic Open n-D Analysis Pipeline



### Introduction (cont.)

- Landmark program is a step [3] pipeline module used for creating and editing a set of landmarks between a reference sample and sample.
- It uses a graphical user interface to let the user interactively assign corresponding spots.
- It saves the landmark set data for a pair of samples in an XML landmark database used by the other Open2Dprot pipeline modules.

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### Initial Open n-D Data-Mining Tools

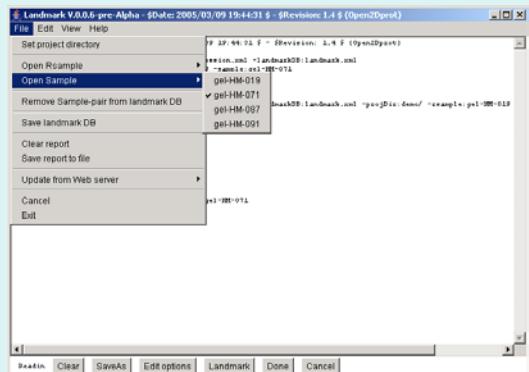
- Accession n-D sample images or n-D data and experiment data
- Quantify 'spots' from sample images or peptide clusters
- Pair spots between samples and a reference sample
- Construct composite sample database for exploratory data analysis
- Manage subsets of proteins in the database
- Manage replicate samples and condition sets of samples
- Analyze expression profiles for multiple conditions
- Data-filter protein sets by statistics, clustering, set membership
- Direct-manipulation of data in graphics, spreadsheets
- Integrate R language statistical, clustering, classifiers, class prediction, and other methods
- Integrate access to Internet proteomic/genomic/function data servers for user-specified protein sets

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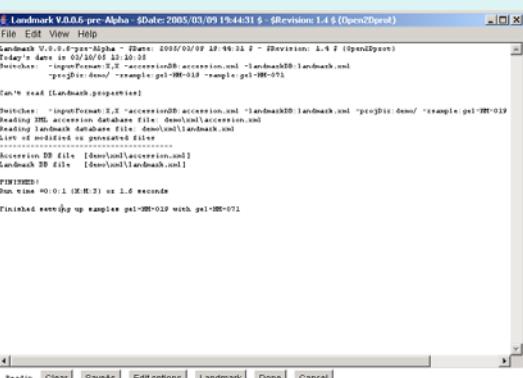
## Open2Dprot Pipeline Subprojects



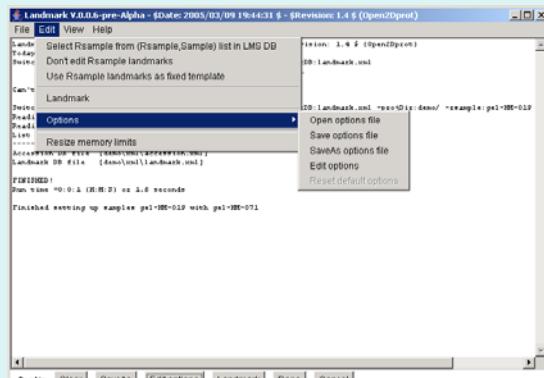
## File Menu - Select Current Sample



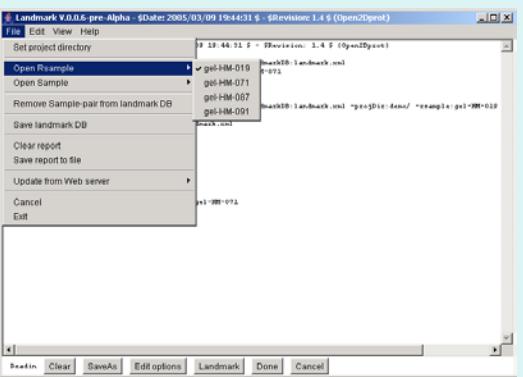
## Main Window



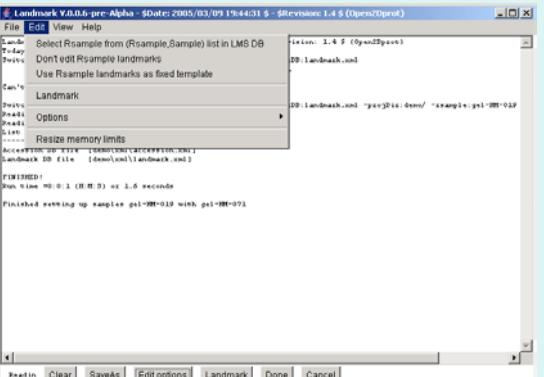
## File Menu - Update From Web Server



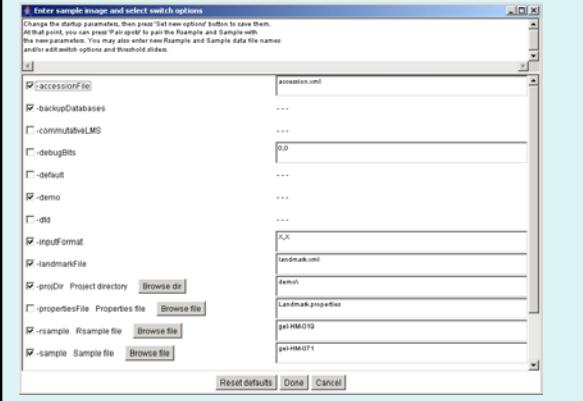
## File Menu - Select Reference Sample



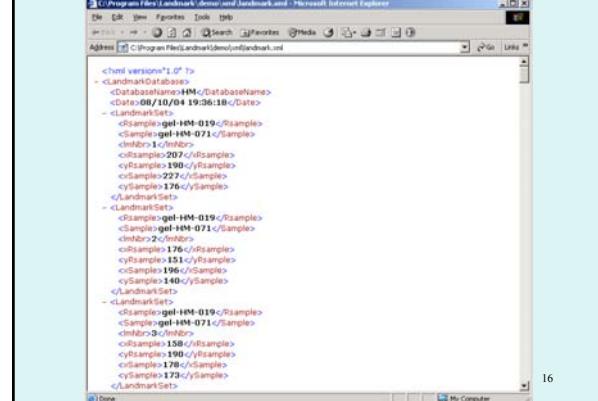
## Edit Menu



## Edit Menu - command line options

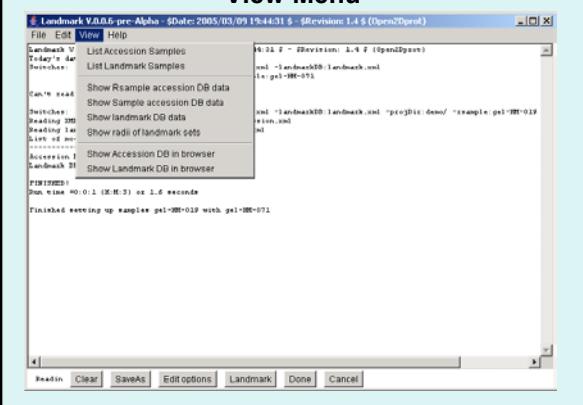


## Landmark XML DB in browser



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## View Menu

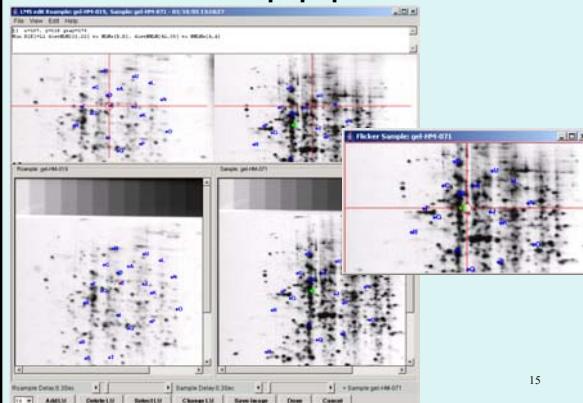


## Summary

- Landmark is a fully open-source landmark spot set editing program and is being developed at <http://open2dprot.sourceforge.net/>
- It uses a graphical user interface to let the user interactively assign corresponding spots.
- It saves the landmark set data for a pair of samples in an XML landmark database used by the other Open2Dprot pipeline modules.

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## Landmark popup window



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